PA   (GETH) GENENTECH INC.
XX
PI   Baker K,   Goddard A,   Gurney AL,   Smith V,   Watanabe CK,   Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   P-PSDB; AAY99362.
XX
PT   New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT   PRO polypeptides, useful for screening of potential peptide or small
PT   molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS   Claim 2; Fig 45; 773pp; English.
XX
CC   AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC   receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC   transmembrane and receptor PRO proteins can be used for screening of
CC   potential peptide or small molecule inhibitors of the relevant
CC   receptor/ligand interactions. The polypeptides and nucleotide sequences
CC   encoding then have various industrial applications, including uses as
CC   pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC   primers and hybridisation probes used in the isolation of the PRO
CC   polypeptides from the present invention
XX
SQ   Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 U; 0 Other;

      Query Match   100.0%;   Score 1989;   DB 3;   Length 1989;
      Best Local Similarity   100.0%;   Pred. No. 0;
      Matches 1989; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTG 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTG 60

Qy   61 CTTTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTTTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAG 120

Qy   121 ACGGACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGC 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGGACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGC 180

Qy   181 CTGGCCGTCCGCCTGGAGGTCACCGACGGCCCCCCGGCCACCCCCGCCTACTGGGACGGC 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGCCGTCCGCCTGGAGGTCACCGACGGCCCCCCGGCCACCCCCGCCTACTGGGACGGC 240

Qy   241 GAGAAGGAGGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGC 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAGAAGGAGGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGC 300

Qy   301 GGGCACGTGTGGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACTGGGACCGG 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCACGTGTGGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACTGGGACCGG 360

Qy   361 CAGCCGCCCGGGGTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAGCCGCCCGGGGTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGC 420

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Qy    421 GAGCGCCGCGCCTACGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCC 480
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Db    421 GAGCGCCGCGCCTACGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCC 480

Qy    481 TTTGAGCGCGGTGACTTCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACC 540
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Db    481 TTTGAGCGCGGTGACTTCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACC 540

Qy    541 TACTCCTGCCACCTGCACCACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTG 600
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Db    541 TACTCCTGCCACCTGCACCACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTG 600

Qy    601 ACGGTCGCCGAACCCCACGCGGAGCCGCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGC 660
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Db    601 ACGGTCGCCGAACCCCACGCGGAGCCGCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGC 660

Qy    661 CACAGCGGCGCCCCAGGCCCAGACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTC 720
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Db    661 CACAGCGGCGCCCCAGGCCCAGACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTC 720

Qy    721 ATCGTCCCCGAGAGCCGAGCCCACTTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCGTCCCCGAGAGCCGAGCCCACTTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTG 780

Qy    781 CTGCTCTTCATCCTGCTACTGGTCACTGTCCTCCTGGCCGCCCGCAGGCGCCGCGGAGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGCTCTTCATCCTGCTACTGGTCACTGTCCTCCTGGCCGCCCGCAGGCGCCGCGGAGGC 840

Qy    841 TACGAATACTCGGACCAGAAGTCGGGAAAGTCAAAGGGGAAGGATGTTAACTTGGCGGAG 900
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Db    841 TACGAATACTCGGACCAGAAGTCGGGAAAGTCAAAGGGGAAGGATGTTAACTTGGCGGAG 900

Qy    901 TTCGCTGTGGCTGCAGGGGACCAGATGCTTTACAGGAGTGAGGACATCCAGCTAGATTAC 960
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Qy    961 AAAAACAACATCCTGAAGGAGAGGGCGGAGCTGGCCCACAGCCCCCTGCCTGCCAAGTAC 1020
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Db    961 AAAAACAACATCCTGAAGGAGAGGGCGGAGCTGGCCCACAGCCCCCTGCCTGCCAAGTAC 1020

Qy   1021 ATCGACCTAGACAAAGGGTTCCGGAAGGAGAACTGCAAATAGGGAGGCCCTGGGCTCCTG 1080
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Db   1021 ATCGACCTAGACAAAGGGTTCCGGAAGGAGAACTGCAAATAGGGAGGCCCTGGGCTCCTG 1080

Qy   1081 GCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTCCTCGGGGCATCTCCTGATGCTCCG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTCCTCGGGGCATCTCCTGATGCTCCG 1140

Qy   1141 GGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCTGGAATTTGGCCTGGGCGTATGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCTGGAATTTGGCCTGGGCGTATGC 1200

Qy   1201 AGAGGCCGCCTCCACACCCCTCCCCCAGGGGCTTGGTGGCAGCATAGCCCCCACCCCTGC 1260
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Db   1201 AGAGGCCGCCTCCACACCCCTCCCCCAGGGGCTTGGTGGCAGCATAGCCCCCACCCCTGC 1260

Qy   1261 GGCCTTTGCTCACGGGTGGCCCTGCCCACCCCTGGCACAACCAAAATCCCACTGATGCCC 1320
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Db    1261 GGCCTTTGCTCACGGGTGGCCCTGCCCACCCCTGGCACAACCAAAATCCCACTGATGCCC 1320

Qy    1321 ATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTGAAGACATTCCTGGAGG 1380
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Qy    1381 ACACTCCCATCAGAACCTGGCAGCCCCAAAACTGGGGTCAGCCTCAGGGCAGGAGTCCCA 1440
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 ACACTCCCATCAGAACCTGGCAGCCCCAAAACTGGGGTCAGCCTCAGGGCAGGAGTCCCA 1440

Qy    1441 CTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCCTGGAGGAGGACACTCCCAT 1500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1501 CAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACTCCTCCTGGGG 1560
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Db    1501 CAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACTCCTCCTGGGG 1560

Qy    1561 TGCTGCCTGCCACCAAGAGCTCCCCCACCTGTACCACCATGTGGGACTCCAGGCACCATC 1620
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Qy    1681 GCCACCTGGGGCTGCACCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTGCTCT 1740
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Db    1681 GCCACCTGGGGCTGCACCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTGCTCT 1740

Qy    1741 CAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTTGG 1800
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Db    1741 CAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTTGG 1800

Qy    1801 ACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA 1860
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Db    1801 ACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA 1860

Qy    1861 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCCACAT 1920
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Db    1861 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCCACAT 1920

Qy    1921 TTGCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAAA 1980
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Qy    1981 AAAAAAAAA 1989
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Db    1981 AAAAAAAAA 1989
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